RAW SEQUENCE LISTING   DATE: 04/23/2002
PATENT APPLICATION: US/09/845,612B   TIME: 08:16:31

Input Set : A:\UTSD795.txt
Output Set: N:\CRF3\04232002\I845612B.raw

```
   3 <110> APPLICANT: YU, HONGTAO
   4        TANG, ZHANYUN
   5        LUO, XUELIAN
   6        RIZO-REY, JOSE
   8 <120> TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTINO OF THE
MITOTIC CHECK
   9        POINT PROTEIN MAD2
  11 <130> FILE REFERENCE: UTSD:795
  13 <140> CURRENT APPLICATION NUMBER: 09/845,612B
  14 <141> CURRENT FILING DATE: 2001-04-27
  16 <160> NUMBER OF SEQ ID NOS: 20
  18 <170> SOFTWARE: PatentIn version 3.0
```

ERRORED SEQUENCES

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  333 <210> SEQ ID NO: 20
  334 <211> LENGTH: 11
  335 <212> TYPE: PRT
  336 <213> ORGANISM: HIV-TAT PROTEIN
  338 <400> SEQUENCE: 20
  340 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
  341 1               5                   10
  343  25025713.1
E--> 344  4
E--> 345  Express Mail No. EH244916502US          — delete
E--> 348  7
E--> 356  UTSD795.txt
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/23/2002
PATENT APPLICATION: US/09/845,612B TIME: 08:16:33

  Input Set : A:\UTSD795.txt
  Output Set: N:\CRF3\04232002\I845612B.raw

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1

VERIFICATION SUMMARY   DATE: 04/23/2002
PATENT APPLICATION: **US/09/845,612B**   TIME: 08:16:33

Input Set : **A:\UTSD795.txt**
Output Set: **N:\CRF3\04232002\I845612B.raw**

L:23 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:344 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:345 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:345 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:4
M:332 Repeated in SeqNo=20
L:356 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:356 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:356 M:252 E: No. of Seq. differs, <211> LENGTH:Input:11 Found:16 SEQ:20